From Debbie Krupke of The Jackson Laboratory

Use Case: A researcher would like to view data from mouse models of mammary adenocarcinoma and compare these data to those collected from patient tumors. He would like to investigate whether or not any of the mouse and human tumors are similar phenotypically and whether or not they carry any common genetic abnormalities.

Query: I want to search for all tumors diagnosed as mammary adenocarcinomas, regardless of the species of origin. The found set of records must contain an image of the tumor and some genetic information. Each tumor must be categorized by organ of origin and by tumor type classification. Standardized gene symbols must be used and links between orthologous genes must exist in the database system. Standard nomenclature for mutations would also be needed for comparison of genetic abnormalities observed in these tumors.

[impacts TPBT, VCDE, clinical trials?, ICR?]